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Cairns et al.

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(54) **SEQUENCES ASSOCIATED WITH TDP-43
PROTEINOPATHIES AND METHODS OF
USING THE SAME**

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(2013.01)
USPC **506/9**; 536/23.5; 530/328; 530/327;
530/326; 530/325; 530/324; 435/6.1; 506/16

(58) **Field of Classification Search**
CPC **C12Q 1/6883**
See application file for complete search history.

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(57) **ABSTRACT**

The present invention provides nucleic acids and peptides,
and methods of using the nucleic acids and peptides to iden-
tify subjects at risk for a TDP-43 proteinopathy. The invention
also provides for an army comprising the nucleic acids and
peptides of the invention.

(56)

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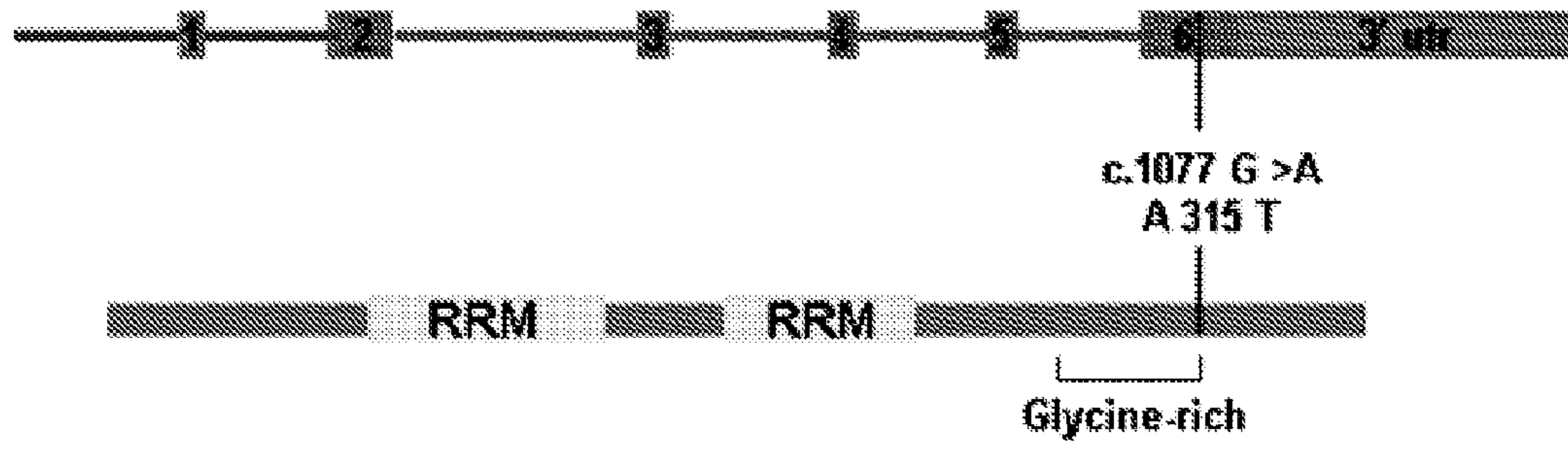
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A



B

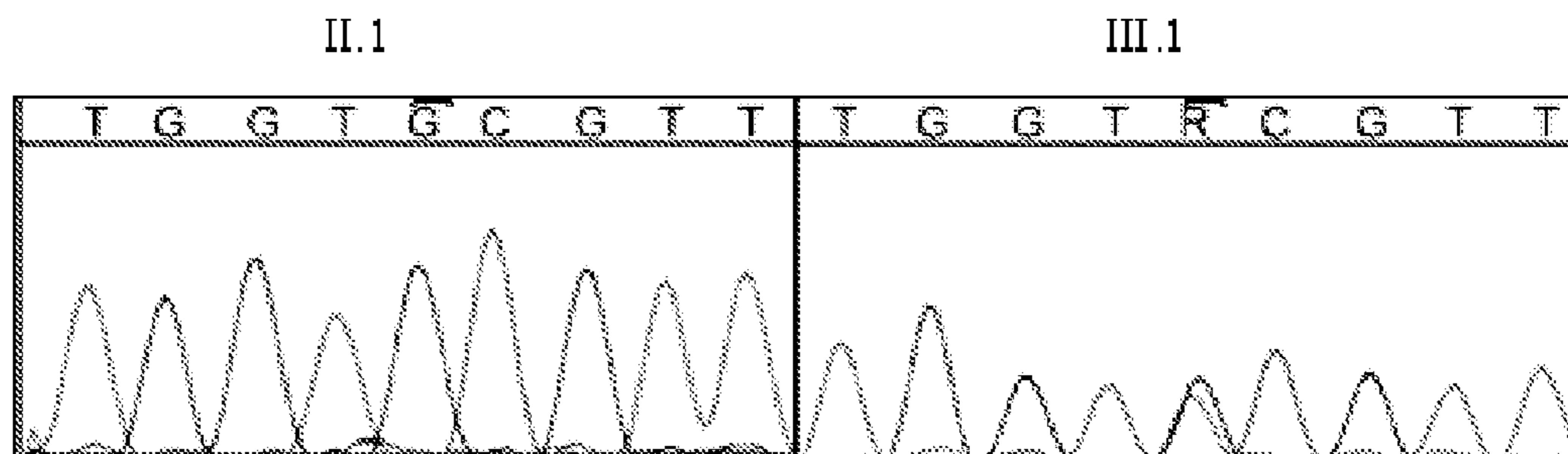


FIG. 1

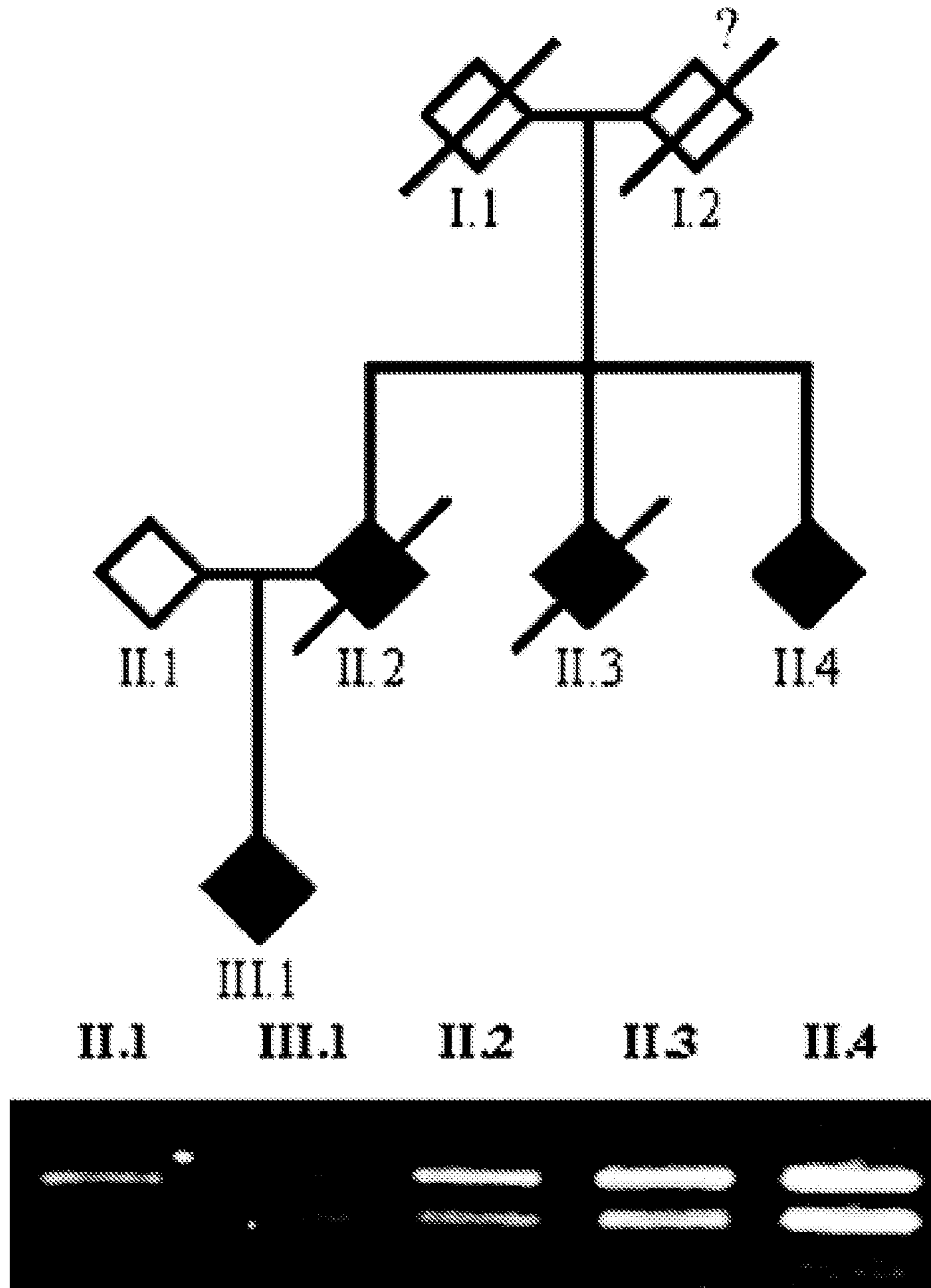


FIG. 1C

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**SEQUENCES ASSOCIATED WITH TDP-43
PROTEINOPATHIES AND METHODS OF
USING THE SAME**

GOVERNMENTAL RIGHTS

This invention was made with government support under P50-AG05681 awarded by the National Institutes of Health. The government has certain rights in the invention.

FIELD OF THE INVENTION

The present invention provides nucleic acid and amino acid sequences that may be utilized to identify subjects at risk for a TDP-43 proteinopathy.

BACKGROUND OF THE INVENTION

TAR DNA-binding protein 43 (TDP-43) is a pathological protein of sporadic and familial frontotemporal lobar degeneration (FTLD) with ubiquitin-positive, tau-negative inclusions (FTLD-U) with or without motor neuron disease (MND). MND is a neurodegenerative disorder involving the loss of upper and/or lower motor neurons and is characterized clinically by progressive weakness and death within a few years of onset; the most common clinical MND phenotype is amyotrophic lateral sclerosis (ALS). Recently, TAR DNA-binding protein 43 (TDP-43) was identified as a pathological protein of the motor neuron inclusions found in sporadic MND, but not in familial MND with Cu/Zn superoxide dismutase-1 (SOD1) mutation.¹⁻⁴ TDP-43 thus defines a class of neurodegenerative diseases referred to as TDP-43 proteinopathies. There is a need in the art for understanding the link between TDP-43 and these diseases, such that diagnostic and therapeutic treatments may be developed.

SUMMARY OF THE INVENTION

One aspect of the invention encompasses an isolated nucleic acid comprising at least ten contiguous nucleotides, including nucleotide 1077, of SEQ ID NO:1.

Another aspect of the invention encompasses an isolated peptide comprising at least ten contiguous amino acids, including amino acid 315, of SEQ ID NO:2.

Yet another aspect of the invention encompasses a method for identifying a subject at risk for a TDP-43 proteinopathy. The method comprises determining the identity of the nucleotide at position 1077 of a nucleotide sequence comprising the nucleic acid sequence of SEQ ID NO:1 in a sample from

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a subject. The presence of a G instead of an A at nucleotide 1077 indicates a risk for a TDP-43 proteinopathy.

An additional aspect of the invention encompasses a method for identifying a subject at risk for a TDP-43 proteinopathy. The method comprises determining the identity of the amino acid at position 315 of an amino acid sequence comprising the amino acid sequence of SEQ ID NO:2 in a sample from a subject. The presence of a threonine instead of an alanine at amino acid 315 indicates a risk for a TDP-43 proteinopathy.

A further aspect of the invention encompasses an array that comprises an address comprising an epitope binding agent. In one iteration, the epitope binding agent can specifically bind to SEQ ID NO:1 or a portion thereof containing nucleotide 1077. Alternatively, the epitope binding agent can specifically bind to SEQ ID NO:2 or a portion thereof containing amino acid 315.

Other aspects and iterations of the invention are described more thoroughly below.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 depicts illustrations showing that the missense mutation A315T within a highly conserved region of exon 6 of TDP-43 segregates with all affected members of an autosomal dominant MND family. (a) TDP-43 genomic structure, position of missense mutation, and location of amino acid change adjacent to glycine-rich domain. (b) Chromatogram of exon 6 displays a base pair change (c.1077 G>A) compared to family control. (c) Pedigree of family displays segregation of the mutation with disease (\diamond =unaffected, \blacklozenge =affected with mutation, diagonal line=deceased). RsaI restriction digest was used to screen family members and 1,505 controls. Direct sequencing was also performed on all family members in this study to verify the mutation.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a nucleic acid sequence variant of TDP-43 (SEQ ID NO:1 in Table 1) that is associated with TDP-43 proteinopathies. In particular, nucleic acid 1077 of SEQ ID NO:1 is an A, as opposed to a G. Additionally, the invention provides an amino acid sequence variant (SEQ ID NO:2 in Table 1) of TDP-43 that is associated with TDP-43 proteinopathies. In particular, amino acid 315 of SEQ ID NO:2 is a threonine, as opposed to an alanine. The invention also encompasses methods of diagnosing or detecting a TDP-43 proteinopathy in a subject and an array. The sequences for SEQ ID Nos. 1, 2, 3, and 4 are shown in Table 1 below.

TABLE 1

SEQ ID NO:	Sequence
1	gggtgggccccgggaggaggcggccctagcgcattttgtgggagcgaagcgggtggctgggctgccc cttgggtccgctcgtgcttccggtgtccctgtcgggcttcccagcagcggcctagcgggaaaagta aaagatgtctgaatatattcgggtaaccgaagatgagaacgatgagccattgaaataccatcgg aagacgatgggacgggtgctgctctccacgggttacagcccagtttccagggcggtggtgggcttcgc tacaggaatccagtgctcagtgatgagaggtgtccggctggtagaaggaattctgcatgcccc agatgctgggctgggaaatctgggtgatgtgtcaactatccaaaagatacaaaaagaaaatgg atgagacagatgcttcatcagcagtgaaagtgaaaagagcagtcagaaaacatccgatttaata gtgttgggtctcccatggaaaacaaccgaacaggacctgaaagagtattttagtacctttggaga agttcttatgggtcagggtcaagaaagatcttaagactgggtcattcaagggggtttggctttgttc gttttacggaatgaaacacaagtgaaagtaatgtcacagcgacatgatagatggacgatgg tgtgactgcaaaacttccataattctaagcaaaagcaagatgagcctttgagaagcagaaaagtgtt tgtggggcgctgtacagaggacatgactgaggatgagctgcccggagtcttctctcagtacgggg atgtgatggatgtcttcatccccaaagccattcagggcctttgectttgttacatttgcagatgat cagattgcccagtcctcttggggagaggacttgatcattaaaggaatcagcgttcatatataccaa tgccgaacctaaagcaaatagcaatagacagttagaaagaagtggaagatttgggtggaatccag gtggctttgggaatcagggtggatttggtaaatagcagaggggggtggagctgggttgggaaacaat caaggtagtaatatgggtgggtgggatgaacttggtagcgttcagcattaatccagccatgatggc tgccgcccaggcagcactacagagcagttggggatgatgggcagtttagccagccagcagaacc

TABLE 1-continued

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agtcaggcccatcgggtaataaccaaaaccaaggcaacatgcagagggagccaaaccaggccttc
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caatgcagggtcgggcagtggttttaattggaggctttggctcaagcatggattctaaagtctctg
gctggggaatgtagacagtggttgggttgggttggatagaatgggtgggaattcaaatttttc
taaactcatggtaagtataatgtaaaatacatatgtactaagaattttcaaaattggtttgttca
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tggtgtcacagtggtttggttctttgttttggtttttaaacactgtctccctcatacacaag
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YFSTFGEVLMVQVKKDLKTGHSKGFVFRFTEYETQVKVMSQRHMDGRWCDCKLPSKQ
SQDEPLRSRKVFVGRCTEDMTEDELEFFFSQYGDVMDVFI PKPFRAFVTFADDQIAQSL
CGEDLI IKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNQ
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TABLE 1-continued

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 aaaaaaaaaa

SEQ ID MSEYIRVTEDENDPEIPISEDDGTVLLSTVTAQFPAGCLRYRNPVSQCMRGVRLVEGILH
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 YFSTFGEVLMVQVKKDLKTGHSKGFVFRFTEYETQVKVMSQRHMIDGRWCDCCLPNSKQ
 SQDEPLRSRKVFGVGRCTEDMTEDELREFFSQYGDVMDVFI PKPFRAFVAVTFADDQIAQSL
 CGEDLI I KGISVHISNAEPKHNSNRQLERSGRFGGNPGGFNGGGFGNSRGGGAGLGNQ
 GSNMGGMNFQAFSINPAMMAAQAALQSSWGMMLASQQNQSGPSGNNQNGNM
 QREPNQAFGSGNNSYSGNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM

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I. Nucleic Acid

One aspect of the present invention encompasses an isolated nucleic acid. Generally speaking, the sequence of the nucleic acid comprises nucleotide position 1077 of SEQ ID NO:1. In particular, the sequence of the nucleic acid comprises an A at position 1077 of SEQ ID NO:1, as opposed to the wild-type sequence that has a G at position 1077 (SEQ ID NO:3, Table 1). In one embodiment, the nucleic acid comprises at least five contiguous nucleotides, including nucleotide 1077, of SEQ ID NO:1. In another embodiment, the nucleic acid comprises at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, or at least 100 contiguous nucleotides, including nucleotide 1077, of SEQ ID NO:1. In yet another embodiment, the nucleic acid comprises at least 200, at least 300, at least 400, at least 500, at least 600, at least 700, at least 800, at least 900, or at least 1000 contiguous nucleotides, including nucleotide 1077, of SEQ ID NO:1. In a further embodiment, the nucleic acid comprises at least 1000, at least 2000, at least 3000, at least 4000, or more than 4000 contiguous nucleotides, including nucleotide 1077, of SEQ ID NO:1.

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In an alternative embodiment, the nucleic acid comprises exon 6 of TDP-43, wherein nucleic acid 1077 is an A instead of a G. In another alternative embodiment, the nucleic acid comprises the cDNA of TDP-43, wherein nucleic acid 1077 is an A instead of a G. In certain embodiments, the nucleic acid consists of the nucleic acid sequence of SEQ ID NO:1.

The present invention also encompasses nucleic acids that are complementary to the isolated nucleic acid sequences described above. For instance, in some embodiments, a nucleic acid of the invention hybridizes to a nucleic acid comprising nucleotide position 1077 of SEQ ID NO:1. In other embodiments, the nucleic acid hybridizes to a nucleic acid comprising nucleotide 1077 of SEQ ID NO:1 but not to a nucleic acid comprising nucleotide 1077 of SEQ ID NO:3. In one embodiment, the nucleic acid hybridizes to a nucleic acid comprising exon 6 of TDP-43, wherein nucleic acid 1077 is an A instead of a G.

Hybridization of nucleic acids is typically performed under stringent conditions. Nucleic acid duplex or hybrid stability is expressed as the melting temperature or T_m , which is the temperature at which a probe dissociates from a target DNA. This melting temperature is used to define the required strin-

gency conditions. To maximize the rate of annealing of the probe with its target, hybridizations are generally carried out at a temperature that is about 20 to 25° C. below the T_m. For instance, stringent conditions may typically involve hybridizing at about 68° C. in 5×SSC/5×Denhardt's solution/1.0% SDS, and washing in 0.2×SSC/0.1% SDS at about 68° C. Moderately stringent conditions include washing in 3×SSC at 42° C. The parameters of salt concentration and temperature can be varied to achieve the optimal level of identity between the nucleic acid and the target sequence, for instance, a sequence comprising nucleotide 1077 of SEQ ID NO:1. One skilled in the art will appreciate which parameters to manipulate to optimize hybridization. Additional guidance regarding such conditions is readily available in the art, for example, by Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, N.Y.; and Ausubel et al., (eds.), 1995, *Current Protocols in Molecular Biology*, (John Wiley & Sons, N.Y.) at Unit 2.10.

The isolated nucleic acids of the invention may be labeled. Non-limiting examples of suitable labels may include fluorescent labels, chemiluminescent labels, radioactive labels, colorimetric labels, and resonance labels. Methods of labeling nucleic acids are well known in the art.

The various nucleic acids mentioned above may be obtained using a variety of different techniques known in the art. The nucleic acids may be isolated using standard techniques, may be synthesized using standard techniques, or may be purchased or obtained from a depository. Once the nucleic acid is obtained, it may be amplified and/or sequenced for use in a variety of applications, e.g. the methods described below.

The invention also encompasses production of nucleic acids comprising nucleotide 1077 of SEQ ID NO:1, or derivatives or fragments thereof, that may be made by any method known in the art, including by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art.

II. Peptide

Another aspect of the present invention encompasses an isolated peptide. Generally speaking, the amino acid sequence of the peptide comprises the amino acid at position 315 of SEQ ID NO:2. In particular, the sequence of the peptide comprises threonine at position 315 of SEQ ID NO:2, as opposed to the wild-type sequence that has an alanine at position 315 (SEQ ID NO:4 in Table 1). In one embodiment, the peptide comprises at least five contiguous amino acids, including amino acid 315, of SEQ ID NO:2. In another embodiment, the peptide comprises at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 90 or at least 100 contiguous amino acids, including amino acid 315, of SEQ ID NO:2. In yet another embodiment, the peptide comprises at least 200, at least 300, at least 400 or at least 500 contiguous amino acids, including amino acid 315, of SEQ ID NO:2.

In an alternative embodiment, the peptide comprises the translated amino acid sequence of exon 6 of TDP-43, wherein amino acid 315 is a threonine. In yet another alternative, the peptide consists of the amino acid sequence of TDP-43, wherein amino acid 315 is a threonine.

The isolated peptide of the invention may be labeled. Non-limiting examples of suitable labels include fluorescent labels, chemiluminescent labels, radioactive labels, colorimetric labels, and resonance labels. Methods of labeling peptides are well known in the art.

The various peptides mentioned above may be obtained using a variety of different techniques known in the art. The peptides may be isolated using standard techniques, may be synthesized using standard techniques, or may be purchased or obtained from a depository.

The invention also encompasses production of peptides comprising amino acid 315 of SEQ ID NO:2, or derivatives or fragments thereof, that may be made by any method known in the art, including by synthetic chemistry.

III. Methods

Yet another aspect of the invention encompasses methods for determining risk and diagnosis of a TDP-43 proteinopathy. As used herein, a TDP-43 proteinopathy is a disorder or a disease characterized in part by a mutation or malfunction of the TDP-43 protein. In an exemplary embodiment, a TDP-43 proteinopathy is a disease or a disorder characterized in part by the substitution of the guanine at nucleotide 1077 of SEQ ID NO:3 to an adenine resulting in the nucleic acid sequence variant of SEQ ID NO:1, or the substitution of the alanine at amino acid 315 of SEQ ID NO:4 to a threonine resulting in the amino acid sequence variant of SEQ ID NO:2. Non-limiting examples of a TDP-43 proteinopathy may include sporadic frontotemporal lobar degeneration (FTLD), also called frontotemporal dementia, familial FTLD, sporadic MND, familial MND, sporadic ALS, and familial ALS, and combinations of these two motor and cognitive phenotypes, including FTLD-MND.

In one embodiment, the invention provides a method for determining whether a subject is at risk for a TDP-43 proteinopathy. For instance, in some embodiments, the invention provides a method for determining whether a subject is at risk for ALS. Generally speaking, the method comprises determining whether the subject has an adenine at nucleotide 1077 of TDP-43 instead of a guanine. If an adenine is present, the subject may be at risk for developing a TDP-43 proteinopathy. Alternatively, the method may comprise determining whether the subject has a threonine at amino acid 315 of TDP-43 instead of an alanine. If a threonine is present, the subject may be at risk for developing a TDP-43 proteinopathy.

In another embodiment, the invention provides a method for diagnosing a subject with a TDP-43 proteinopathy. For instance, in some embodiments, the invention provides a method for diagnosing a subject with ALS. Typically, the method comprises determining whether the subject has an adenine at nucleotide 1077 of TDP-43 instead of a guanine. If an adenine is present, the subject may be diagnosed with a TDP-43 proteinopathy. Alternatively, the method may comprise determining whether the subject has a threonine at amino acid 315 of TDP-43 instead of an alanine. If a threonine is present, the subject may be diagnosed with a TDP-43 proteinopathy.

Methods for determining whether a subject has an adenine at nucleotide 1077 of TDP-43 instead of a guanine are known in the art. For instance, sequencing of a portion of TDP-43 encompassing nucleotide 1077 may be performed as detailed in the examples. Alternatively, an array may be used as detailed below.

In certain embodiments, nucleic acid from a subject may be digested with a restriction enzyme that generates a unique fragment in a subject with an adenine at nucleotide 1077 of TDP-43 instead of a guanine. For instance, the restriction enzyme *Rsa*I may be used. *Rsa*I generates a unique fragment when incubated with a nucleic acid comprising exon 6 of TDP-43 when nucleotide 1077 is an adenine. The fragment may be amplified from genomic DNA using the polymerase chain reaction method. For instance, see FIG. 1C.

Similarly, methods for determining whether a subject has a threonine at amino acid 315 of TDP-43 instead of an alanine are known in the art. For instance, an array may be used as detailed below. Alternatively an antibody that recognizes a threonine at position 315, but not an alanine, may be used.

Methods of obtaining a nucleic acid and/or a peptide of the invention from a subject are known in the art. For instance, biological samples comprising a nucleic acid and/or a peptide of the invention may be collected from a subject. Non-limiting examples of suitable biological samples may include blood samples, tissues samples, or bodily fluid samples. Blood samples may include whole blood, serum, or plasma. Bodily fluid samples may include urine, lymph, or saliva samples.

Suitable subjects express TDP-43. For instance, humans, non-human primates, rodents, livestock animals, and companion animals are non-limiting examples of suitable subjects. Rodents may include mice, rats, and guinea pigs. Livestock animals may include cattle, swine, and chicken. Companion animals may include cats and dogs. In some embodiments, the subject is a frog. In each of the above embodiments, the subject may have a family history of a TDP-43 proteinopathy, of a MND, or of FTLD. Alternatively, the subject may have symptoms of a TDP-43 proteinopathy, of a MND, or of a FTLD. In some embodiments, the subject may have no clinical symptoms of a TDP-43 proteinopathy, of a MND, or of a FTLD.

IV. Array

A further aspect of the invention is an array comprising at least one address. In some embodiments, at least one address of the array has disposed thereon an epitope binding agent that can specifically bind to SEQ ID NO:1, or a portion thereof, containing nucleotide 1077. In other embodiments, at least one address of the array has disposed thereon an epitope binding agent that can specifically bind to SEQ ID NO: 2, or a portion thereof, containing amino acid 315.

Several substrates suitable for the construction of arrays are known in the art, and one skilled in the art will appreciate that other substrates may become available as the art progresses. The substrate may be a material that may be modified to contain discrete individual sites appropriate for the attachment or association of an epitope binding agent and is amenable to at least one detection method. Non-limiting examples of substrate materials include glass, modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), nylon or nitrocellulose, polysaccharides, nylon, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses and plastics. In an exemplary embodiment, the substrate may allow optical detection without appreciably fluorescing.

A substrate may be planar, a substrate may be a well, i.e. a 364 well plate, or alternatively, a substrate may be a bead. Additionally, the substrate may be the inner surface of a tube for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

An epitope binding agent may be attached to the substrate in a wide variety of ways, as will be appreciated by those in the art. The nucleic acid or epitope binding agent may either be synthesized first, with subsequent attachment to the substrate, or may be directly synthesized on the substrate. The substrate and the epitope binding agent may be derivatized with chemical functional groups for subsequent attachment of the two. For example, the substrate may be derivatized with

a chemical functional group including, but not limited to, amino groups, carboxyl groups, oxo groups or thiol groups. Using these functional groups, the epitope binding agent may be attached using functional groups on the nucleic acid or epitope binding agent either directly or indirectly using linkers.

The epitope binding agent may also be attached to the substrate non-covalently. For example, a biotinylated epitope binding agent may be prepared, which may bind to surfaces covalently coated with streptavidin, resulting in attachment. Alternatively, an epitope binding agent may be synthesized on the surface using techniques such as photopolymerization and photolithography. Additional methods of attaching epitope binding agents to arrays and methods of synthesizing biomolecules on substrates are well known in the art, i.e. VLSIPS technology from Affymetrix (e.g., see U.S. Pat. No. 6,566,495, and Rockett and Dix, *Xenobiotica* 30(2):155-177, both of which are hereby incorporated by reference in their entirety).

In one embodiment, the epitope binding agent attached to the substrate is located at a spatially defined address of the array. Arrays may comprise from about 1 to about several hundred thousand addresses. In one embodiment, the array may be comprised of less than 10,000 addresses. In another alternative embodiment, the array may be comprised of at least 10,000 addresses. In yet another alternative embodiment, the array may be comprised of less than 5,000 addresses. In still another alternative embodiment, the array may be comprised of at least 5,000 addresses. In a further embodiment, the array may be comprised of less than 500 addresses. In yet a further embodiment, the array may be comprised of at least 500 addresses.

An epitope binding agent may be represented more than once on a given array. In other words, more than one address of an array may be comprised of the same epitope binding agent. In some embodiments, two, three, or more than three addresses of the array may be comprised of the same epitope binding agent. In certain embodiments, the array may comprise control epitope binding agents and/or control addresses. The controls may be internal controls, positive controls, negative controls, or background controls.

As used herein, "epitope binding agent" may refer to a nucleic acid, an oligonucleic acid, an amino acid, a peptide, a polypeptide, a protein, a lipid, a metabolite, a small molecule or a fragment thereof that recognizes and is capable of binding to SEQ ID NO: 2 or a portion thereof containing amino acid 315, or to SEQ ID NO:1 or a portion thereof containing nucleic acid 1077. Nucleic acids may include RNA, DNA, and naturally occurring or synthetically created derivatives.

In further embodiments, an epitope binding agent of the array may recognize mutations in one or more of the sequences selected from the group of sequences comprising the vesicle-associated membrane protein-associated protein B (VAPB), dynactin (DCTN 1), alsin (ALS2), immunoglobulin μ binding protein 2 (IGHMBP2), or glycyl-tRNA synthetase (GARS) genes that are associated with MND.

The arrays may be utilized in several suitable applications. For example, the arrays may be used in methods for detecting association between an epitope binding agent and a target. As used herein, "target" refers to a nucleic acid comprising nucleotide 1077 of SEQ ID NO:1 or a peptide comprising amino acid 315 of SEQ ID NO:2. This method typically comprises incubating a sample comprising a target with the array under conditions such that the target may associate with the epitope binding agent attached to the array. The association may then be detected, using means commonly known in the art, such as fluorescence. "Association," as used in this

context, may refer to hybridization, covalent binding, or ionic binding. A skilled artisan will appreciate that conditions under which association may occur will vary depending on the epitope binding agent, the substrate, the sample, and the detection method utilized. As such, suitable conditions may have to be optimized for each individual array created.

In yet another embodiment, the array may be used as a tool in a method for determining whether a subject is at risk for developing a TDP-43 proteinopathy. Similarly, the array may be used as a tool in a method for determining whether a subject is at risk for a MND. Alternatively, the array may be used as a tool in a method for determining whether a subject is at risk for ALS. In another alternative, the array may be used as a tool in a method for determining whether a subject is at risk for FTLD. Typically, such a method comprises incubating the array with a biological sample from the subject. If the biological sample comprises a nucleic acid comprising nucleotide 1077 of SEQ ID NO:1, or a peptide comprising amino acid 315 of SEQ ID NO:2, then an association between the array and the sample may be detected, and the subject may be at risk for developing a TDP-43 proteinopathy.

In certain embodiments, the array may be used as a tool in a method for diagnosing a subject with a TDP-43 proteinopathy. Similarly, the array may be used as a tool in a method for diagnosing a subject with a MND. Alternatively, the array may be used as a tool in a method for diagnosing a subject with ALS. In another alternative, the array may be used as a tool in a method for diagnosing a subject with a FTLD. Typically, such a method comprises incubating the array with a biological sample from the subject. If the biological sample comprises a nucleic acid comprising nucleotide 1077 of SEQ ID NO:1, or a peptide comprising amino acid 315 of SEQ ID NO:2, then an association between the array and the sample may be detected, and the subject may be diagnosed with a TDP-43 proteinopathy.

In each of the above embodiments, the subject may not display clinical signs of MND, ALS, or FTLD. In some embodiments, the subject may display only a few clinical signs of MND, ALS or FTLD.

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples that follow represent techniques discovered by the inventors to function well in the practice of the invention. Those of skill in the art should, however, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments that are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention, therefore all matter set forth or shown in the accompanying drawings is to be interpreted as illustrative and not in a limiting sense.

EXAMPLES

The following examples illustrate various iterations of the invention.

Methods

Genetic Analysis.

High molecular weight DNA was extracted from whole blood, serum or brain tissue according to standard procedures. DNA from serum was whole-genome amplified using the REPLI-g® Midi Kit (Qiagen Inc., Valencia, Calif., USA) prior to genetic analysis. DNA from a single affected individual from each family was used for sequencing of TDP-43. All exons and the intron-exon boundaries of the TDP-43 gene were amplified using gene specific intronic primers. Direct sequencing of the amplified fragments was performed using the Big Dye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Wellesley, Mass., USA) and standard protocols. For most of the fragments the primers used for

sequencing were the same as those used for PCR amplification. Reactions were run on an ABI3130 and mutation analysis was performed using Sequencher software v4.6 (Gene Codes Corporation, Ann Arbor, Mich., USA). Positive calls for sequence variants were made only if the variant was observed in both forward and reverse sequence reads. Where possible, sequence variants were tested for segregation with the disease and screened in a set of 1,505 unrelated ethnically-matched controls.

Example 1

Screening

Mutation analysis of the TDP-43 gene was undertaken in 8 families with MND/ALS with an autosomal dominant pattern of inheritance and no mutation within the SOD1 gene, 5 families with familial FTLD-MND, and 25 families with FTLD-U.¹⁴ All families were of European descent. No sporadic cases of MND were available, but additional sporadic cases of FTLD-MND (n=6) and FTLD-U (n=28) were investigated.

This analysis led to the identification of a missense mutation, Ala-315-Thr (c.1077G>A) within exon 6. In TDP-43 this alanine residue is highly conserved throughout the evolutionary spectrum from *Homo sapiens* to *Xenopus tropicalis*, supporting its likely functional importance (Table 2). The A315T mutation segregated with all affected members of an autosomal dominant MND family (additional non-coding sequence variants were also identified in cases with FTLD-U, FTLD-MND, and MND see FIG. 1b & c and Table 3). This mutation was absent from a large series of ethnically matched elderly controls (n=1,505).

The phenotype of the four affected family members with the TDP-43 A315T mutation involved a slowly progressive lower motor neuron degeneration syndrome with respiratory involvement, with only minimal involvement of upper motor or bulbar neurons and absence of dementia (Table 3). Brain autopsy in this kindred remains to be undertaken. Similar clinical phenotypes have been reported in sporadic MND and in kindreds with SOD1 mutations.^{5,6} The TDP-43 mutation in familial MND reported here supplements other familial neurodegenerative conditions that affect predominantly lower motor neurons including mutations in the vesicle-associated membrane protein-associated protein B (VAPB), dynactin (DCTN1), alsin (ALS2), immunoglobulin μ binding protein 2 (IGHMBP2), and glycyl-tRNA synthetase (GARS) genes, and other mutations in juvenile MND, although some of these mutations have been identified in motor neuron diseases and hereditary motor neuropathies with variable clinical phenotypes.¹⁵

These data have important implications for both sporadic and familial forms of MND and FTLD-U, which are linked by a common molecular pathology: TDP-43 proteinopathy. The discovery of a missense mutation in TDP-43 in a family with dominantly inherited MND provides evidence of a direct link between TDP-43 function and neurodegeneration.

Example 2

Clinical Family Analysis

The proband (subject III-1 of FIG. 1d) developed weakness and atrophy of his right hand at age 48 years. Leg strength, mental status, cranial nerves, sensory examination, reflexes, coordination and gait were normal at initial examination; upper motor neuron findings were absent. Motor and sensory nerve conduction was normal, but electromyography (EMG) showed denervation in the arms both proximally and distally, with fasciculation potentials in the legs, and occa-

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sional large motor unit potentials. Magnetic resonance imaging (MRI) of brain and spinal cord were normal, as was blood work including absent anti-GM1 antibodies; SOD1 gene testing was normal. Three years later his upper extremity weakness had progressed but mental status, cranial nerve function, leg strength, and sensation remained normal.

The proband's father (subject II-2) developed a left foot drop at age 72. Exam showed atrophy and distal weakness in the left foot, fasciculations, and increased deep tendon reflexes without other abnormalities. EMG revealed widespread fasciculations with denervation changes in the legs and paraspinal muscles. Weakness steadily progressed to involve all four extremities with respiratory and swallowing difficulty, and he died of respiratory compromise seven years after diagnosis.

Subject II-3 developed left foot drop at age 64, which progressed to involve both legs and his arms within two years.

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Examination at age 69 showed symmetric proximal and distal weakness in the upper extremities, with asymmetric (left>right) distal predominant weakness in the legs. Reflexes were brisk throughout. Electrophysiology showed normal sensory and motor nerve conduction, with denervation changes in both the upper and lower extremities. Respiratory weakness developed at age 72 years, and he died of respiratory complications at age 73 years.

Subject II-4 developed right leg weakness at age 83, which progressed to involve both legs requiring wheelchair dependence within two years. Asymmetric arm weakness and respiratory weakness developed at age 85 and at age 86 there was severe atrophy and weakness in the lower and upper extremities with widespread fasciculations.

For more details, see Table 4.

TABLE 2

TDP-43 protein (291-340 amino acids) displays high similarity between species. Residues underlined indicate differences when compared to humans. TDP-43 A315T location is indicated in bold italic.

Species	291-340	SEQ. ID NO.
<i>Homo sapiens</i>	NSRGGGAGLGNNQGSNM - - GGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	5
<i>Pan troglodytes</i>	NSRGGGAGLGNNQGSNM - - GGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	6
<i>Macaca mulatta</i>	NSRGGGAGLGNNQGSNM - - GGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	7
<i>Bos Taurus</i>	NSRGGGAGLGNNQGSNM - - GGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	8
<i>Felis catus</i>	NSRGGGAGLGNNQGSNM - - GGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	9
<i>Cavia porcellus</i>	N-RGGGAGLGNNQGSNM - - GGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	10
<i>Rattus norvegicus</i>	NSRGGGAGLGNNQGGNM - - GGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	11
<i>Mus musculus</i>	NSRGGGAGLGNNQGGNM - - GGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	12
<i>Gallus gallus</i>	NSRGGGGGLGNNQGSNM - - GGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	13
<i>Xenopus tropicalis</i>	NSR <u>PSS</u> GALGNNQGGNMGGGGMNF <i>GA</i> FSINPAMMAAAQAALQSSWGMMGML	14

TABLE 3

Position	Region	Nucleotide change	Amino acid	Pathological entities	Frequency
c.1-430	5'UTR	G > A	n/a	MND	0.04a
c.332	Ex 2	T > C	A 66 A	MND, FTLD-MND, control	0.01087b
c.848 + 69	In 5-6	+G	n/a	MND, FTLD-MND, FTLD-U, control	0.25c
c.1077	Ex 6	G > A	A 315 T	MND	0.0003d
c.2076	3'UTR	G > A	n/a	MND, FTLD-U	0.0072e
c.3674	3'UTR	+GTTTT	n/a	MND, FTLD-MND, FTLD-U, control	0.8409f

(numbering corresponds to polymorphism location with respect to NM_007375); Frequency based on number of chromosomes screened (a) 60/1,390, (b) 3/276, (c) 19/76, (d) 1/3,010, (e) 2/276, (f) 37/44). With 276 chromosomes screened and a population frequency of 1%, the power to detect a variant is 0.94.

TABLE 4

Clinical features of a family with MND with a TDP-43 A315T variant.								
Subject	Age at onset/ death (years)	Clinical findings					Electrophysiology	
		Mental status	Cranial nerves	Respiratory involvement	Site of onset	Disease course	Nerve conductions (age performed)	Electromyography
II-2	72/79	Normal	Normal	Yes	Left lower extremity	Progressive asymmetric lower motor neuron loss in legs before arms, distal before proximal. Brisk reflexes. Death from respiratory weakness.	Normal SNAP amplitudes, normal sensory and motor velocities (72)	Fibs/PSW in legs, thoracic paraspinal muscles. Reduced recruitment. Occasional large motor units. Fasciculations throughout.
II-3	64/74	Normal	Normal	Yes	Left lower extremity	Progressive asymmetric lower motor neuron loss in legs before arms, distal and proximal. Brisk reflexes. Death from respiratory weakness.	Normal SNAP amplitudes, normal sensory and motor velocities (68)	Fibs/PSW in legs and arms. Reduced recruitment. Occasional large motor units. Fasciculations throughout.
II-4	83	Normal	Normal	Yes	Right lower extremity	Progressive asymmetric lower motor neuron loss, distal and proximal, legs before arms. Brisk reflexes.	Not available	Not available
III-1	48	Normal	Normal	No	Right upper extremity	Progressive asymmetric lower motor neuron loss, distal before proximal, arms before legs.	Normal SNAP amplitudes, normal sensory and motor velocities (49)	Fibs/PSW in arms. Fasciculations in arms/legs

Fibs = fibrillations; PSW = positive sharp waves; SNAP = sensory nerve action potential.

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SEQUENCE LISTING

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tttttttga caccacaaaa aaaaaaaaaa aaaaaa 4236

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<210> SEQ ID NO 2

<211> LENGTH: 414

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

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Met Ser Glu Tyr Ile Arg Val Thr Glu Asp Glu Asn Asp Glu Pro Ile
1           5           10           15

Glu Ile Pro Ser Glu Asp Asp Gly Thr Val Leu Leu Ser Thr Val Thr
20           25           30

Ala Gln Phe Pro Gly Ala Cys Gly Leu Arg Tyr Arg Asn Pro Val Ser
35           40           45

Gln Cys Met Arg Gly Val Arg Leu Val Glu Gly Ile Leu His Ala Pro
50           55           60

Asp Ala Gly Trp Gly Asn Leu Val Tyr Val Val Asn Tyr Pro Lys Asp
65           70           75           80

Asn Lys Arg Lys Met Asp Glu Thr Asp Ala Ser Ser Ala Val Lys Val
85           90           95

Lys Arg Ala Val Gln Lys Thr Ser Asp Leu Ile Val Leu Gly Leu Pro
100          105          110

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Trp	Lys	Thr	Thr	Glu	Gln	Asp	Leu	Lys	Glu	Tyr	Phe	Ser	Thr	Phe	Gly
		115					120					125			
Glu	Val	Leu	Met	Val	Gln	Val	Lys	Lys	Asp	Leu	Lys	Thr	Gly	His	Ser
	130					135					140				
Lys	Gly	Phe	Gly	Phe	Val	Arg	Phe	Thr	Glu	Tyr	Glu	Thr	Gln	Val	Lys
145					150					155					160
Val	Met	Ser	Gln	Arg	His	Met	Ile	Asp	Gly	Arg	Trp	Cys	Asp	Cys	Lys
			165						170					175	
Leu	Pro	Asn	Ser	Lys	Gln	Ser	Gln	Asp	Glu	Pro	Leu	Arg	Ser	Arg	Lys
			180					185					190		
Val	Phe	Val	Gly	Arg	Cys	Thr	Glu	Asp	Met	Thr	Glu	Asp	Glu	Leu	Arg
		195					200					205			
Glu	Phe	Phe	Ser	Gln	Tyr	Gly	Asp	Val	Met	Asp	Val	Phe	Ile	Pro	Lys
	210					215					220				
Pro	Phe	Arg	Ala	Phe	Ala	Phe	Val	Thr	Phe	Ala	Asp	Asp	Gln	Ile	Ala
225					230					235					240
Gln	Ser	Leu	Cys	Gly	Glu	Asp	Leu	Ile	Ile	Lys	Gly	Ile	Ser	Val	His
				245					250					255	
Ile	Ser	Asn	Ala	Glu	Pro	Lys	His	Asn	Ser	Asn	Arg	Gln	Leu	Glu	Arg
			260					265					270		
Ser	Gly	Arg	Phe	Gly	Gly	Asn	Pro	Gly	Gly	Phe	Gly	Asn	Gln	Gly	Gly
		275					280					285			
Phe	Gly	Asn	Ser	Arg	Gly	Gly	Gly	Ala	Gly	Leu	Gly	Asn	Asn	Gln	Gly
	290					295					300				
Ser	Asn	Met	Gly	Gly	Gly	Met	Asn	Phe	Gly	Thr	Phe	Ser	Ile	Asn	Pro
305					310					315					320
Ala	Met	Met	Ala	Ala	Ala	Gln	Ala	Ala	Leu	Gln	Ser	Ser	Trp	Gly	Met
			325						330					335	
Met	Gly	Met	Leu	Ala	Ser	Gln	Gln	Asn	Gln	Ser	Gly	Pro	Ser	Gly	Asn
			340					345					350		
Asn	Gln	Asn	Gln	Gly	Asn	Met	Gln	Arg	Glu	Pro	Asn	Gln	Ala	Phe	Gly
		355					360					365			
Ser	Gly	Asn	Asn	Ser	Tyr	Ser	Gly	Ser	Asn	Ser	Gly	Ala	Ala	Ile	Gly
	370					375					380				
Trp	Gly	Ser	Ala	Ser	Asn	Ala	Gly	Ser	Gly	Ser	Gly	Phe	Asn	Gly	Gly
385					390					395					400
Phe	Gly	Ser	Ser	Met	Asp	Ser	Lys	Ser	Ser	Gly	Trp	Gly	Met		
				405					410						

<210> SEQ ID NO 3

<211> LENGTH: 4236

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

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gggaaaagta aaagatgtct gaatatattc ggtaaccga agatgagaac gatgagccca      180
ttgaaatacc atcggaagac gatgggacgg tgctgctctc cacggttaca gccagtttc      240
caggggcgtg tgggcttcgc tacaggaatc cagtgtctca gtgtatgaga ggtgtccggc      300
tggtagaagg aattctgcat gcccagatg ctggctgggg aaatctggtg tatgttgtca      360
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aaacacaagt	gaaagtaatg	tcacagcgac	atatgataga	tggacgatgg	tgtgactgca	660
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<210> SEQ ID NO 4

<211> LENGTH: 414

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

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Met Ser Glu Tyr Ile Arg Val Thr Glu Asp Glu Asn Asp Glu Pro Ile
1           5           10           15
Glu Ile Pro Ser Glu Asp Asp Gly Thr Val Leu Leu Ser Thr Val Thr
20           25           30
Ala Gln Phe Pro Gly Ala Cys Gly Leu Arg Tyr Arg Asn Pro Val Ser
35           40           45
Gln Cys Met Arg Gly Val Arg Leu Val Glu Gly Ile Leu His Ala Pro
50           55           60
Asp Ala Gly Trp Gly Asn Leu Val Tyr Val Val Asn Tyr Pro Lys Asp
65           70           75           80
Asn Lys Arg Lys Met Asp Glu Thr Asp Ala Ser Ser Ala Val Lys Val
85           90           95
Lys Arg Ala Val Gln Lys Thr Ser Asp Leu Ile Val Leu Gly Leu Pro
100          105          110
Trp Lys Thr Thr Glu Gln Asp Leu Lys Glu Tyr Phe Ser Thr Phe Gly

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115					120					125					
Glu	Val	Leu	Met	Val	Gln	Val	Lys	Lys	Asp	Leu	Lys	Thr	Gly	His	Ser
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Lys	Gly	Phe	Gly	Phe	Val	Arg	Phe	Thr	Glu	Tyr	Glu	Thr	Gln	Val	Lys
145					150					155					160
Val	Met	Ser	Gln	Arg	His	Met	Ile	Asp	Gly	Arg	Trp	Cys	Asp	Cys	Lys
				165					170					175	
Leu	Pro	Asn	Ser	Lys	Gln	Ser	Gln	Asp	Glu	Pro	Leu	Arg	Ser	Arg	Lys
			180					185					190		
Val	Phe	Val	Gly	Arg	Cys	Thr	Glu	Asp	Met	Thr	Glu	Asp	Glu	Leu	Arg
		195					200					205			
Glu	Phe	Phe	Ser	Gln	Tyr	Gly	Asp	Val	Met	Asp	Val	Phe	Ile	Pro	Lys
210					215					220					
Pro	Phe	Arg	Ala	Phe	Ala	Phe	Val	Thr	Phe	Ala	Asp	Asp	Gln	Ile	Ala
225				230					235						240
Gln	Ser	Leu	Cys	Gly	Glu	Asp	Leu	Ile	Ile	Lys	Gly	Ile	Ser	Val	His
				245					250					255	
Ile	Ser	Asn	Ala	Glu	Pro	Lys	His	Asn	Ser	Asn	Arg	Gln	Leu	Glu	Arg
			260					265					270		
Ser	Gly	Arg	Phe	Gly	Gly	Asn	Pro	Gly	Gly	Phe	Gly	Asn	Gln	Gly	Gly
		275					280					285			
Phe	Gly	Asn	Ser	Arg	Gly	Gly	Gly	Ala	Gly	Leu	Gly	Asn	Asn	Gln	Gly
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305					310					315					320
Ala	Met	Met	Ala	Ala	Ala	Gln	Ala	Ala	Leu	Gln	Ser	Ser	Trp	Gly	Met
				325					330					335	
Met	Gly	Met	Leu	Ala	Ser	Gln	Gln	Asn	Gln	Ser	Gly	Pro	Ser	Gly	Asn
			340					345					350		
Asn	Gln	Asn	Gln	Gly	Asn	Met	Gln	Arg	Glu	Pro	Asn	Gln	Ala	Phe	Gly
			355				360					365			
Ser	Gly	Asn	Asn	Ser	Tyr	Ser	Gly	Ser	Asn	Ser	Gly	Ala	Ala	Ile	Gly
				370			375					380			
Trp	Gly	Ser	Ala	Ser	Asn	Ala	Gly	Ser	Gly	Ser	Gly	Phe	Asn	Gly	Gly
385					390					395					400
Phe	Gly	Ser	Ser	Met	Asp	Ser	Lys	Ser	Ser	Gly	Trp	Gly	Met		
				405					410						

<210> SEQ ID NO 5
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

Asn	Ser	Arg	Gly	Gly	Gly	Ala	Gly	Leu	Gly	Asn	Asn	Gln	Gly	Ser	Asn
1				5					10					15	
Met	Gly	Gly	Gly	Met	Asn	Phe	Gly	Ala	Phe	Ser	Ile	Asn	Pro	Ala	Met
			20					25					30		
Met	Ala	Ala	Ala	Gln	Ala	Ala	Leu	Gln	Ser	Ser	Trp	Gly	Met	Met	Gly
			35				40					45			
Met	Leu														
	50														

<210> SEQ ID NO 6
 <211> LENGTH: 50

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<212> TYPE: PRT
 <213> ORGANISM: Pan troglodytes

<400> SEQUENCE: 6

Asn Ser Arg Gly Gly Gly Ala Gly Leu Gly Asn Asn Gln Gly Ser Asn
 1 5 10 15

Met Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro Ala Met
 20 25 30

Met Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met Met Gly
 35 40 45

Met Leu
 50

<210> SEQ ID NO 7
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Macaca mulatta

<400> SEQUENCE: 7

Asn Ser Arg Gly Gly Gly Ala Gly Leu Gly Asn Asn Gln Gly Ser Asn
 1 5 10 15

Met Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro Ala Met
 20 25 30

Met Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met Met Gly
 35 40 45

Met Leu
 50

<210> SEQ ID NO 8
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Bos taurus

<400> SEQUENCE: 8

Asn Ser Arg Gly Gly Gly Ala Gly Leu Gly Asn Asn Gln Gly Ser Asn
 1 5 10 15

Met Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro Ala Met
 20 25 30

Met Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met Met Gly
 35 40 45

Met Leu
 50

<210> SEQ ID NO 9
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Felis catus

<400> SEQUENCE: 9

Asn Ser Arg Gly Gly Gly Ala Gly Leu Gly Asn Asn Gln Gly Ser Asn
 1 5 10 15

Met Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro Ala Met
 20 25 30

Met Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met Met Gly
 35 40 45

Met Leu
 50

<210> SEQ ID NO 10

-continued

<211> LENGTH: 49
 <212> TYPE: PRT
 <213> ORGANISM: *Cavia porcellus*

<400> SEQUENCE: 10

Asn Arg Gly Gly Gly Ala Gly Leu Gly Asn Asn Gln Gly Ser Asn Met
 1 5 10 15

Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro Ala Met Met
 20 25 30

Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met Met Gly Met
 35 40 45

Leu

<210> SEQ ID NO 11
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: *Rattus norvegicus*

<400> SEQUENCE: 11

Asn Ser Arg Gly Gly Gly Ala Gly Leu Gly Asn Asn Gln Gly Gly Asn
 1 5 10 15

Met Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro Ala Met
 20 25 30

Met Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met Met Gly
 35 40 45

Met Leu
 50

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<400> SEQUENCE: 12

Asn Ser Arg Gly Gly Gly Ala Gly Leu Gly Asn Asn Gln Gly Gly Asn
 1 5 10 15

Met Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro Ala Met
 20 25 30

Met Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met Met Gly
 35 40 45

Met Leu
 50

<210> SEQ ID NO 13
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: *Gallus gallus*

<400> SEQUENCE: 13

Asn Ser Arg Gly Gly Gly Gly Gly Leu Gly Asn Asn Gln Gly Ser Asn
 1 5 10 15

Met Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro Ala Met
 20 25 30

Met Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met Met Gly
 35 40 45

Met Leu
 50

<210> SEQ ID NO 14

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<211> LENGTH: 52
<212> TYPE: PRT
<213> ORGANISM: Xenopus tropicalis

<400> SEQUENCE: 14

Asn Ser Arg Pro Ser Ser Gly Ala Leu Gly Asn Asn Gln Gly Gly Asn
1           5           10           15
Met Gly Gly Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro
          20           25           30
Ala Met Met Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met
          35           40           45
Met Gly Met Leu
          50

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What is claimed is:

1. A method for detecting a mutation in a TDP-43 gene 20 from a human subject, comprising
- (i) obtaining a sample comprising a TDP-43 gene from the human subject; and
 - (ii) sequencing the TDP-43 gene; and
 - (iii) detecting an adenine at a position corresponding to 25 position 1077 of SEQ ID NO:1.
2. A method for identifying a human subject at risk for a TDP-43 proteinopathy, comprising (i) obtaining a sample 30 comprising a TDP-43 gene from the human subject; (ii) sequencing the TDP-43 gene; (iii) detecting an adenine at a position corresponding to position 1077 of SEQ ID NO:1; and (iv) identifying the subject as having a risk for a TDP-43 proteinopathy when an adenine is detected at position 1077 of SEQ ID NO:1.
3. The method of claim 2, wherein the subject is also at risk 35 for motor neuron disease (MND) selected from the group consisting of familial MND and amyotrophic lateral sclerosis (ALS).
4. The method of claim 2, wherein the subject is also at risk for FTL-D-U.
5. A method for classifying a human subject with FTL-D-U or MND as having a TDP-43 proteinopathy, comprising
- (i) obtaining a sample comprising a TDP-43 gene from the human subject;
 - (ii) sequencing the TDP-43 gene;
 - (iii) detecting an adenine at a position corresponding to 40 position 1077 of SEQ ID NO:1; and
 - (iv) identifying the subject as having a TDP-43 proteinopathy when an adenine is detected at a position corresponding to position 1077 of SEQ ID NO:1.
6. The method of claim 5, wherein the MND is selected from the group consisting of familial MND and ALS.
7. A method for classifying a human subject with familial MND as having a TDP-43 proteinopathy, comprising
- (i) obtaining a sample comprising a TDP-43 gene from the human subject;
 - (ii) sequencing the TDP-43 gene;
 - (iii) detecting an adenine at a position corresponding to 45 position 1077 of SEQ ID NO:1; and
 - (iv) identifying the subject as having a TDP-43 proteinopathy when an adenine is detected at a position corresponding to position 1077 of SEQ ID NO:1.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 8,889,597 B2
APPLICATION NO. : 12/865659
DATED : November 18, 2014
INVENTOR(S) : Nigel J. Cairns et al.

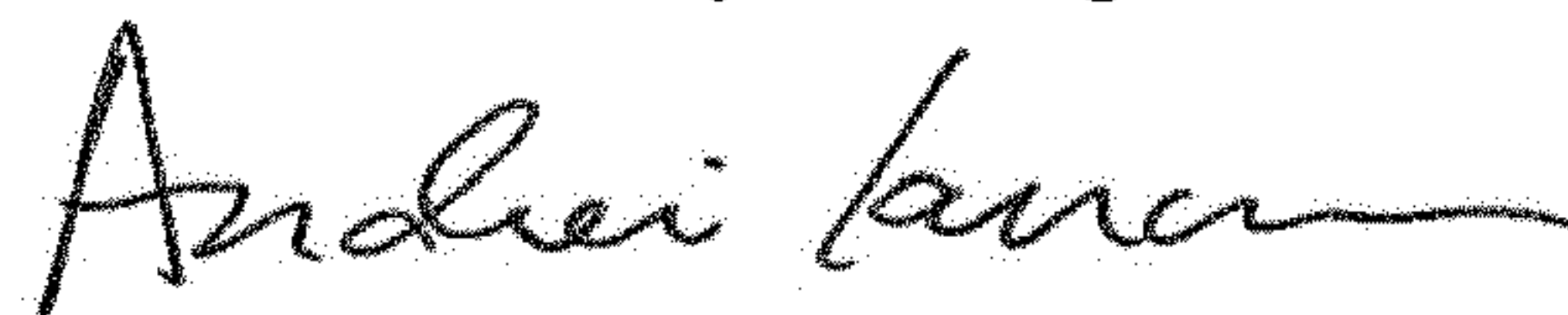
Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the Specification

At Column 1, Lines 7-9: "This invention was made with government support under P50-AG-5681 awarded by the National Institutes of Health. The government has certain rights in the invention." should read "This invention was made with government support under AG005681 awarded by the National Institutes of Health. The government has certain rights in the invention."

Signed and Sealed this
Twentieth Day of August, 2019



Andrei Iancu
Director of the United States Patent and Trademark Office